DNA SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 07:26:51 ; Search time 5556 Seconds
                                (without alignments)
                                10742.145 Million cell updates/sec

Title: US-09-955-315-1
Perfect score: 1377
Sequence: 1 gggtgcgctctgcatcggtg..........aatcgcctctaagggcctaa 1377

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1:   gb_ba:*
                2:   gb_htg:*
                3:   gb_in:*
                4:   gb_om:*
                5:   gb_ov:*
                6:   gb_pat:*
                7:   gb_ph:*
                8:   gb_pl:*
                9:   gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*
                15: em_ba:*
                16: em_fun:*
                17: em_hum:*
                18: em_in:*
                19: em_mu:*
                20: em_om:*
                21: em_or:*
                22: em_ov:*
                23: em_pat:*
                24: em_ph:*
                25: em_pl:*
                26: em_ro:*
                27: em_sts:*

*Searched SEQ 1 (DNA)
        2 (encoded PROT)

in DNA databases.*

Also searched oligos

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1377	100.0	1377	6	AX405298	AX405298 Sequence
c	2	1377	100.0	309400	6	AX127153	AX127153 Sequence
c	3	1377	100.0	325651	1	AP005283	AP005283 Corynebac
	4	495	35.9	495	6	AX123403	AX123403 Sequence
	5	495	35.9	495	6	BD165520	BD165520 Novel pol
c	6	426.8	31.0	302070	1	AP005223	AP005223 Corynebac
c	7	358	26.0	813	6	AX123404	AX123404 Sequence
c	8	358	26.0	813	6	BD165521	BD165521 Novel pol
c	9	314.2	22.8	349659	1	BX248360	BX248360 Corynebac
	10	176.4	12.8	552	1	AY065628	AY065628 Mycobacte
	11	169.8	12.3	4611	1	AF068267	AF068267 Streptomy
	12	169.8	12.3	314100	1	SCO939106	AL939106 Streptomy
	13	119.4	8.7	780	1	HDU18769	U18769 Haemophilus
c	14	119.4	8.7	304558	1	AE017151	AE017151 Haemophil
	15	118	8.6	10517	1	AE014683	AE014683 Bifidobac
	16	118	8.6	349980	6	AX492783	AX492783 Sequence
	17	118	8.6	349980	6	AX553950	AX553950 Sequence
	18	95.6	6.9	3657	1	CGPTAACKA	X89084 C.glutamicu
c	19	95.6	6.9	320550	1	AP005282	AP005282 Corynebac
c	20	95.6	6.9	349980	6	AX127152	AX127152 Sequence
	21	86	6.2	309400	6	AX127153	AX127153 Sequence
	22	86	6.2	325651	1	AP005283	AP005283 Corynebac
	23	86	6.2	349980	6	AX127152	AX127152 Sequence
c	24	81.2	5.9	326150	1	AP005281	AP005281 Corynebac
c	25	81.2	5.9	349980	6	AX127150	AX127150 Sequence
	26	74.2	5.4	531	6	AR388806	AR388806 Sequence
	27	74.2	5.4	340000	1	AP005274	AP005274 Corynebac
	28	74.2	5.4	349980	6	AX120085	AX120085 Sequence
	29	71	5.2	10146	1	AE009194	AE009194 Agrobacte
	30	71	5.2	10161	1	AE008160	AE008160 Agrobacte
	31	70.2	5.1	307050	1	BX294140	BX294140 Pirellula
	32	70	5.1	504	1	AY195736	AY195736 Klebsiell
c	33	68.4	5.0	299550	1	AP005031	AP005031 Streptomy

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 02:55:31 ; Search time 593 Seconds
                                              (without alignments)
                                              9864.703 Million cell updates/sec

Title: US-09-955-315-1
Perfect score: 1377
Sequence: 1 gggtgcgctctgcatcggtg..........aatcgcctctaagggcctaa 1377

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002s:*
                  7: geneseqn2003as:*
                  8: geneseqn2003bs:*
                  9: geneseqn2003cs:*
                  10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                  %
Result   Query
    No.   Score Match Length DB ID   Description
    ----
      1   1377 100.0   1377 6 ABL56907   Abl56907 Corynebac
  c   2   1377 100.0 309400 5 AAH68534   Aah68534 C glutami
      3   495   35.9   495 5 AAH68284   Aah68284 C glutami
      4   495   35.9   495 7 ACA00504   Aca00504 C. glutam
  c   5   441   32.0   441 7 ACA00503   Aca00503 C. glutam
  c   6   358   26.0   813 5 AAH68285   Aah68285 C glutami
  c   7   352   25.6   807 7 ACA00505   Aca00505 C. glutam
      8   273.6   19.9   483 7 ACA29828   Aca29828 Prokaryot

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 10:12:17 ; Search time 116 Seconds
                                      (without alignments)
                                      6587.650 Million cell updates/sec

Title: US-09-955-315-1
Perfect score: 1377
Sequence: 1 gggtgcgctctgcatcggtg..........aatcgcctctaagggcctaa 1377

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score Match Length DB   ID   Description
   ----
       1   74.2   5.4   531   4   US-09-489-039A-5535   Sequence 5535, Ap
       2   67   4.9   534   4   US-09-543-681A-987   Sequence 987, App
       3   55.6   4.0   483   4   US-09-252-991A-12631   Sequence 12631, A
       4   45.4   3.3   501   4   US-09-134-001C-1366   Sequence 1366, Ap
       5   40.4   2.9   315   2   US-08-889-013C-5   Sequence 5, Appli
c   6   39   2.8 1830121   4   US-09-557-884-1   Sequence 1, Appli
c   7   39   2.8 1830121   4   US-09-643-990A-1   Sequence 1, Appli
       8   38   2.8   564   4   US-09-543-681A-150   Sequence 150, App
c   9   38   2.8   6436   4   US-09-600-099-1   Sequence 1, Appli
      10   37   2.7   468   4   US-09-252-991A-16447   Sequence 16447, A
c   11   37   2.7   516   4   US-09-252-991A-16153   Sequence 16153, A
c   12   35.6   2.6   2889   4   US-09-016-434-1192   Sequence 1192, Ap

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 12:11:12 ; Search time 515 Seconds
                                          (without alignments)
                                          9362.649 Million cell updates/sec

Title: US-09-955-315-1
Perfect score: 1377
Sequence: 1 gggtgcgctctgcatcggtg..........aatcgcctctaagggcctaa 1377

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
          1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
          2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
          3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
          4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
          5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
          6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
          7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
          8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
         10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
         11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
         12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
         13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
         14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
         15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
         16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
         17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
         18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

```
                              SUMMARIES
                    %
Result            Query
    No.   Score   Match Length DB   ID                        Description
      ---------------------------------------------------------------------------------
      1    1377   100.0   1377   9   US-09-955-315-1           Sequence 1, Appli
c     2    1377   100.0 3309400  9   US-09-738-626-1           Sequence 1, Appli
      3     495    35.9   495    9   US-09-738-626-3319        Sequence 3319, Ap
c     4     358    26.0   813    9   US-09-738-626-3320        Sequence 3320, Ap
      5   273.6    19.9   483   12   US-10-282-122A-17698      Sequence 17698, A
      6   176.4    12.8   546   12   US-10-282-122A-25586      Sequence 25586, A
      7      86     6.2 3309400  9   US-09-738-626-1           Sequence 1, Appli
      8    74.2     5.4   501   12   US-10-282-122A-23746      Sequence 23746, A
      9    68.4     5.0   468   14   US-10-156-761-2491        Sequence 2491, Ap
c    10    68.4     5.0 9025608  14   US-10-156-761-1          Sequence 1, Appli
     11    66.6     4.8   501   12   US-10-282-122A-19300      Sequence 19300, A
     12    66.4     4.8   504   12   US-10-282-122A-41603      Sequence 41603, A
     13      62     4.5   486   12   US-10-282-122A-14089      Sequence 14089, A
     14    61.8     4.5   501   12   US-10-282-122A-36886      Sequence 36886, A
     15    60.2     4.4   504   12   US-10-282-122A-39666      Sequence 39666, A
c    16    59.6     4.3  1364   9   US-09-826-909-1           Sequence 1, Appli
     17    58.8     4.3   504   12   US-10-282-122A-20306      Sequence 20306, A
     18    58.4     4.2   480   14   US-10-156-761-1594        Sequence 1594, Ap
     19    58.4     4.2 9025608  14   US-10-156-761-1          Sequence 1, Appli
c    20    57.8     4.2   177    9   US-09-738-626-2911        Sequence 2911, Ap
     21    55.6     4.0   471    9   US-09-815-242-7717        Sequence 7717, Ap
     22    55.6     4.0   471   12   US-10-282-122A-30051      Sequence 30051, A
     23    54.4     4.0   648   12   US-10-282-122A-13139      Sequence 13139, A
     24    52.8     3.8   486   12   US-10-282-122A-11558      Sequence 11558, A
c    25    51.2     3.7   807   14   US-10-156-761-5411        Sequence 5411, Ap
     26    45.4     3.3   444   12   US-10-282-122A-34931      Sequence 34931, A
c    27    45.2     3.3  1377   9   US-09-955-315-1           Sequence 1, Appli
     28      44     3.2   436   12   US-10-282-122A-10758      Sequence 10758, A
     29      44     3.2   438   12   US-10-282-122A-10356      Sequence 10356, A
     30    42.8     3.1   558   12   US-10-282-122A-15143      Sequence 15143, A
     31    42.6     3.1   471   12   US-10-282-122A-33816      Sequence 33816, A
     32    40.4     2.9  2559   12   US-10-282-122A-6960       Sequence 6960, Ap
     33    40.2     2.9   471   12   US-10-282-122A-31929      Sequence 31929, A
     34    40.2     2.9   480   12   US-10-282-122A-30920      Sequence 30920, A
     35    39.6     2.9   174    9   US-09-738-626-449         Sequence 449, App
     36    39.2     2.8   415   12   US-10-282-122A-22988      Sequence 22988, A
     37      39     2.8   483    9   US-09-815-242-7134        Sequence 7134, Ap
     38      39     2.8   483   12   US-10-282-122A-22313      Sequence 22313, A
c    39      39     2.8 1830121  14   US-10-329-960-1          Sequence 1, Appli
c    40      39     2.8 1830121  15   US-10-329-670-1          Sequence 1, Appli
     41    38.6     2.8   444    9   US-09-815-242-8271        Sequence 8271, Ap
     42    38.6     2.8   444   12   US-10-282-122A-7708       Sequence 7708, Ap
c    43    38.4     2.8   932   12   US-10-424-599-11756       Sequence 11756, A
     44      38     2.8   552   12   US-10-282-122A-33024      Sequence 33024, A
     45    37.6     2.7   426    9   US-09-815-242-4498        Sequence 4498, Ap


                              ALIGNMENTS


RESULT 1
US-09-955-315-1
```

```
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OM nucleic - nucleic search, using sw model

Run on:           February 21, 2004, 10:09:38 ; Search time 3900 Seconds
                                     (without alignments)
                                     10543.647 Million cell updates/sec


Title:            US-09-955-315-1
Perfect score:    1377
Sequence:         1 gggtgcgctctgcatcggtg..........aatcgcctctaagggcctaa 1377


Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


Searched:         27513289 seqs, 14931090276 residues


Total number of hits satisfying chosen parameters:      55026578


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        EST:*
                  1:  em_estba:*
                  2:  em_esthum:*
                  3:  em_estin:*
                  4:  em_estmu:*
                  5:  em_estov:*
                  6:  em_estpl:*
                  7:  em_estro:*
                  8:  em_htc:*
                  9:  gb_est1:*
                  10: gb_est2:*
                  11: gb_htc:*
                  12: gb_est3:*
                  13: gb_est4:*
                  14: gb_est5:*
                  15: em_estfun:*
                  16: em_estom:*
                  17: em_gss_hum:*
                  18: em_gss_inv:*
                  19: em_gss_pln:*
                  20: em_gss_vrt:*
                  21: em_gss_fun:*
                  22: em_gss_mam:*
                  23: em_gss_mus:*
                  24: em_gss_pro:*
                  25: em_gss_rod:*
                  26: em_gss_phg:*
                  27: em_gss_vrl:*
                  28: gb_gss1:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	59.4	4.3	636	14	CF841965	CF841965 psHB017xA
c	2	58.8	4.3	679	14	CF851308	CF851308 psMA019xF
c	3	58.8	4.3	693	14	CF841926	CF841926 psHB016xM
c	4	58.8	4.3	694	14	CF851254	CF851254 psMA019xB
c	5	58.8	4.3	705	14	CF851365	CF851365 psMA019xH
c	6	52	3.8	579	14	CF754444	CF754444 EST-77-2-
c	7	49.6	3.6	742	12	BJ619993	BJ619993 BJ619993
c	8	45.6	3.3	350	9	AU251612	AU251612 AU251612
	9	45.4	3.3	743	28	BZ562850	BZ562850 pacs2-164
c	10	44.2	3.2	607	12	BM415829	BM415829 OP20911 M
	11	44	3.2	669	13	CA092935	CA092935 SCCCCL100
	12	43	3.1	597	12	BM415925	BM415925 OP21007 M
	13	43	3.1	736	9	AU168008	AU168008 AU168008
	14	42.8	3.1	842	28	BZ571864	BZ571864 msh2_2090
	15	41.6	3.0	801	12	BG825420	BG825420 602746830
c	16	41.4	3.0	506	12	BJ191550	BJ191550 BJ191550
c	17	41.2	3.0	589	12	BM415853	BM415853 OP20935 M
c	18	40.4	2.9	927	28	AZ692740	AZ692740 ENTKY30TF
c	19	40.2	2.9	369	14	W66612	W66612 me23b10.r1
	20	40	2.9	1168	13	BX386385	BX386385 BX386385
c	21	39.2	2.8	566	6	AL814237	Al814237 Triticum
	22	39	2.8	1201	13	BX381961	BX381961 BX381961
	23	38.6	2.8	765	12	BG340063	BG340063 602438227
c	24	38.6	2.8	1284	14	CA207626	CA207626 SCEQSB1C1
	25	38.4	2.8	454	13	BQ252468	BQ252468 san76a09.
	26	38.4	2.8	482	13	BQ295817	BQ295817 sao27c02.
	27	38.4	2.8	525	12	BM094323	BM094323 saj14a09.
	28	38.4	2.8	844	28	BZ571748	BZ571748 msh2_2038
c	29	38.2	2.8	388	10	AW661443	AW661443 833006B05
c	30	38.2	2.8	664	28	BZ563917	BZ563917 pacs2-164
	31	38.2	2.8	682	12	BG450547	BG450547 NF031A06D
c	32	38.2	2.8	915	29	CG901851	CG901851 ZMMBBb051
	33	38.2	2.8	3137	11	BC009370	BC009370 Homo sapi
c	34	37.6	2.7	985	29	CNS03SP8	AL258821 Tetraodon
c	35	37.6	2.7	989	13	BU345760	BU345760 603524814
c	36	37.6	2.7	1159	29	CNS015XR	AL106041 Drosophil
c	37	37.2	2.7	885	13	BX425603	BX425603 BX425603
	38	37	2.7	510	14	CF841740	CF841740 psHB015xM
	39	37	2.7	562	13	BQ801298	BQ801298 WHE2812_G
	40	37	2.7	690	29	CNS0040D	AL054318 Drosophil
c	41	37	2.7	692	29	CC940028	CC940028 ZMMBBb023
c	42	37	2.7	877	28	BZ177450	BZ177450 CH230-443
	43	37	2.7	982	28	CC452499	CC452499 ZMMBBc034
	44	36.8	2.7	450	14	CA666218	CA666218 wlk1.pk00
c	45	36.8	2.7	465	9	AA835142	AA835142 ak63g06.s

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:17:56 ; Search time 3496 Seconds
                                             (without alignments)
                                             2045.652 Million cell updates/sec

Title: US-09-955-315-2
Perfect score: 865
Sequence: 1 MANYTVPGINENDAKQLIDG..........EKFQWFIRAHIVDVDGNIQE 165

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09955315/runat_19022004_145901_28329/app_query.fasta_1.3
27
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09955315_@CGN_1_1_2496_@runat_19022004_145901_28329 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

```
11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
15:  em_ba:*
16:  em_fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mu:*
20:  em_om:*
21:  em_or:*
22:  em_ov:*
23:  em_pat:*
24:  em_ph:*
25:  em_pl:*
26:  em_ro:*
27:  em_sts:*
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	865	100.0	495	6	AX123403	AX123403 Sequence
	2	865	100.0	495	6	BD165520	BD165520 Novel pol
	3	865	100.0	1377	6	AX405298	AX405298 Sequence
c	4	865	100.0	309400	6	AX127153	AX127153 Sequence
c	5	865	100.0	325651	1	AP005283	AP005283 Corynebac
c	6	690	79.8	302070	1	AP005223	AP005223 Corynebac
c	7	657	76.0	349659	1	BX248360	BX248360 Corynebac
	8	470	54.3	552	1	AY065628	AY065628 Mycobacte
	9	432	49.9	4611	1	AF068267	AF068267 Streptomy
	10	432	49.9	314100	1	SCO939106	AL939106 Streptomy
	11	364	42.1	780	1	HDU18769	U18769 Haemophilus
c	12	364	42.1	304558	1	AE017151	AE017151 Haemophil
	13	328.5	38.0	10517	1	AE014683	AE014683 Bifidobac
	14	328.5	38.0	349980	6	AX492783	AX492783 Sequence
	15	328.5	38.0	349980	6	AX553950	AX553950 Sequence
	16	264	30.5	534	6	AR375981	AR375981 Sequence

```
                         GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          February 21, 2004, 19:17:25 ; Search time 370 Seconds
                                             (without alignments)
                                             1894.467 Million cell updates/sec

Title:           US-09-955-315-2
Perfect score:   865
Sequence:        1 MANYTVPGINENDAKQLIDG..........EKFQWFIRAHIVDVDGNIQE 165

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:       6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09955315/runat_19022004_145901_28319/app_query.fasta_1.3
27
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09955315_@CGN_1_1_470_@runat_19022004_145901_28319 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_29Jan04:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002s:*
                 7:  geneseqn2003as:*
                 8:  geneseqn2003bs:*
                 9:  geneseqn2003cs:*
                 10:  geneseqn2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	865	100.0	495	5	AAH68284	Aah68284 C glutami
	2	865	100.0	495	7	ACA00504	Aca00504 C. glutam
	3	865	100.0	1377	6	ABL56907	Abl56907 Corynebac
c	4	865	100.0	309400	5	AAH68534	Aah68534 C glutami
	5	657	76.0	483	7	ACA29828	Aca29828 Prokaryot
	6	459	53.1	546	7	ACA37716	Aca37716 Prokaryot
	7	328.5	38.0	349980	6	ABQ81845	Abq81845 Bifidobac
	8	261	30.2	501	7	ACA49016	Aca49016 Prokaryot
	9	261	30.2	504	7	ACA51796	Aca51796 Prokaryot
	10	247	28.6	501	7	ACA35876	Aca35876 Prokaryot
	11	246	28.4	504	7	ACA32436	Aca32436 Prokaryot
	12	245	28.3	501	7	ACA31430	Aca31430 Prokaryot
	13	240	27.7	1206	5	AAS82058	Aas82058 DNA encod
	14	233	26.9	504	7	ACA53733	Aca53733 Prokaryot
c	15	204	23.6	441	7	ACA00503	Aca00503 C. glutam
	16	199	23.0	29139	4	AAS59569	Aas59569 Propionib
	17	199	23.0	29139	7	ACF64498	Acf64498 Propionib
	18	182	21.0	438	7	ACA47774	Aca47774 Prokaryot
	19	180	20.8	110000	7	ACF67367_16	Continuation (17 o
	20	180	20.8	210710	7	ACF65380	Acf65380 Photorhab
	21	179	20.7	438	7	ACA22486	Aca22486 Prokaryot
	22	175	20.2	415	7	ACA35118	Aca35118 Prokaryot
	23	169	19.5	444	7	ACA47061	Aca47061 Prokaryot
	24	169	19.5	486	7	ACA23688	Aca23688 Prokaryot
c	25	169	19.5	2962	4	AAH54147	Aah54147 S. epider
	26	168	19.4	471	7	ACA44059	Aca44059 Prokaryot
	27	167.5	19.4	444	4	AAS54634	Aas54634 Staphyloc
	28	166	19.2	426	4	AAS51916	Aas51916 Staphyloc
	29	165.5	19.1	441	7	ACF73436	Acf73436 Staphyloc
	30	165.5	19.1	444	7	ACA19838	Aca19838 Prokaryot
	31	163	18.8	501	6	ABN91903	Abn91903 Staphyloc
c	32	161	18.6	110000	6	ABA90521_20	Continuation (21 o
c	33	161	18.6	110000	6	ABA90521_21	Continuation (22 o
	34	160	18.5	525	7	ACA47978	Aca47978 Prokaryot
	35	160	18.5	660	6	AAL41884	Aal41884 Streptoco
c	36	159.5	18.4	17075	6	ABL56780	Abl56780 Nucleotid
	37	159	18.4	471	7	ACA45946	Aca45946 Prokaryot
	38	159	18.4	480	9	ADC91885	Adc91885 E. faeciu
	39	157	18.2	486	7	ACA26219	Aca26219 Prokaryot
	40	156	18.0	648	7	ACA25269	Aca25269 Prokaryot
	41	155	17.9	348	7	ACF68866	Acf68866 Photorhab
	42	155	17.9	465	7	ACA32822	Aca32822 Prokaryot
	43	155	17.9	525	6	ABN70095	Abn70095 Streptoco
	44	155	17.9	528	7	ACA50604	Aca50604 Prokaryot
	45	152	17.6	436	7	ACA22888	Aca22888 Prokaryot

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:21:16 ; Search time 75 Seconds
                                        (without alignments)
                                        1220.892 Million cell updates/sec

Title: US-09-955-315-2
Perfect score: 865
Sequence: 1 MANYTVPGINENDAKQLIDG..........EKFQWFIRAHIVDVDGNIQE 165

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09955315/runat_19022004_145902_28366/app_query.fasta_1.3
27
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09955315_@CGN_1_1_56_@runat_19022004_145902_28366 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	264	30.5	534	4	US-09-543-681A-987	Sequence 987, App
	2	247	28.6	531	4	US-09-489-039A-5535	Sequence 5535, Ap
	3	163	18.8	501	4	US-09-134-001C-1366	Sequence 1366, Ap
c	4	160	18.5	5301	4	US-08-956-171E-443	Sequence 443, App
	5	159	18.4	480	4	US-09-107-532A-1512	Sequence 1512, Ap
	6	151	17.5	483	4	US-09-252-991A-12631	Sequence 12631, A
c	7	142.5	16.5	21040	4	US-08-961-527-55	Sequence 55, Appl
c	8	134.5	15.5	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	9	134.5	15.5	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	10	133.5	15.4	315	2	US-08-889-013C-5	Sequence 5, Appli
	11	122.5	14.2	564	4	US-09-543-681A-150	Sequence 150, App
	12	114.5	13.2	576	4	US-09-107-532A-1728	Sequence 1728, Ap
	13	85	9.8	3048	1	US-08-188-228-47	Sequence 47, Appl
	14	85	9.8	3048	1	US-08-332-643-41	Sequence 41, Appl
	15	85	9.8	3048	1	US-08-332-638-47	Sequence 47, Appl
	16	83	9.6	1845	4	US-09-543-681A-2894	Sequence 2894, Ap
c	17	83	9.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	18	83	9.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	19	82	9.5	1422	4	US-09-252-991A-10517	Sequence 10517, A
c	20	81.5	9.4	1208	4	US-09-205-258-25	Sequence 25, Appl
	21	81	9.4	2022	4	US-09-328-352-1708	Sequence 1708, Ap
	22	79.5	9.2	1203	4	US-09-134-001C-1483	Sequence 1483, Ap
	23	79	9.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	24	78	9.0	1020	4	US-09-107-532A-1490	Sequence 1490, Ap
c	25	77	8.9	957	4	US-09-369-247-56	Sequence 56, Appl
	26	77	8.9	1476	1	US-08-489-733-4	Sequence 4, Appli
	27	77	8.9	1476	2	US-08-993-581B-4	Sequence 4, Appli
	28	77	8.9	1727	3	US-08-999-733-2	Sequence 2, Appli
	29	77	8.9	9757	1	US-08-093-453B-1	Sequence 1, Appli
	30	77	8.9	9759	1	US-08-459-041A-1	Sequence 1, Appli
	31	77	8.9	9759	3	US-08-999-733-1	Sequence 1, Appli
	32	76	8.8	1554	4	US-09-134-001C-2607	Sequence 2607, Ap
	33	75.5	8.7	1398	4	US-09-489-039A-1374	Sequence 1374, Ap
	34	75.5	8.7	1932	4	US-09-252-991A-1911	Sequence 1911, Ap
	35	75.5	8.7	2505	4	US-09-252-991A-1830	Sequence 1830, Ap
c	36	75	8.7	642	4	US-09-370-838-119	Sequence 119, App
c	37	75	8.7	808	4	US-09-023-655-1279	Sequence 1279, Ap
	38	75	8.7	2368	4	US-09-343-011B-3	Sequence 3, Appli
	39	75	8.7	4539	4	US-09-328-352-1037	Sequence 1037, Ap
	40	74.5	8.6	873	4	US-09-252-991A-2784	Sequence 2784, Ap
	41	74.5	8.6	1468	2	US-09-074-512-2	Sequence 2, Appli
c	42	74.5	8.6	1536	4	US-09-252-991A-3182	Sequence 3182, Ap
	43	74.5	8.6	2070	4	US-09-252-991A-2687	Sequence 2687, Ap
	44	74.5	8.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	45	74.5	8.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-543-681A-987
; Sequence 987, Application US/09543681A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 20:33:27 ; Search time 328 Seconds
                                              (without alignments)
                                              1761.498 Million cell updates/sec

Title: US-09-955-315-2
Perfect score: 865
Sequence: 1 MANYTVPGINENDAKQLIDG.........EKFQWFIRAHIVDVDGNIQE 165

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09955315/runat_19022004_145904_28498/app_query.fasta_1.3
27
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09955315_@CGN_1_1_57_@runat_19022004_145904_28498
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

```
12:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:  /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	865	100.0	495	9	US-09-738-626-3319	Sequence 3319, Ap
	2	865	100.0	1377	9	US-09-955-315-1	Sequence 1, Appli
c	3	865	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
	4	657	76.0	483	12	US-10-282-122A-17698	Sequence 17698, A
	5	459	53.1	546	12	US-10-282-122A-25586	Sequence 25586, A
	6	261	30.2	501	12	US-10-282-122A-36886	Sequence 36886, A
	7	261	30.2	504	12	US-10-282-122A-39666	Sequence 39666, A
	8	247	28.6	501	12	US-10-282-122A-23746	Sequence 23746, A
	9	246	28.4	504	12	US-10-282-122A-20306	Sequence 20306, A
	10	245	28.3	501	12	US-10-282-122A-19300	Sequence 19300, A
	11	233	26.9	504	12	US-10-282-122A-41603	Sequence 41603, A
	12	231	26.7	468	14	US-10-156-761-2491	Sequence 2491, Ap
c	13	231	26.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
	14	227.5	26.3	480	14	US-10-156-761-1594	Sequence 1594, Ap
	15	227.5	26.3	9025608	14	US-10-156-761-1	Sequence 1, Appli
	16	182	21.0	438	12	US-10-282-122A-35644	Sequence 35644, A
	17	179	20.7	438	12	US-10-282-122A-10356	Sequence 10356, A
	18	175	20.2	415	12	US-10-282-122A-22988	Sequence 22988, A
	19	169	19.5	444	12	US-10-282-122A-34931	Sequence 34931, A
	20	169	19.5	486	12	US-10-282-122A-11558	Sequence 11558, A
	21	168	19.4	471	12	US-10-282-122A-31929	Sequence 31929, A
	22	167.5	19.4	444	9	US-09-815-242-8271	Sequence 8271, Ap
	23	166	19.2	426	9	US-09-815-242-4498	Sequence 4498, Ap
	24	165.5	19.1	444	12	US-10-282-122A-7708	Sequence 7708, Ap
	25	160	18.5	525	12	US-10-282-122A-35848	Sequence 35848, A
c	26	160	18.5	5301	8	US-08-781-986A-443	Sequence 443, App
	27	159	18.4	471	12	US-10-282-122A-33816	Sequence 33816, A
	28	157	18.2	486	12	US-10-282-122A-14089	Sequence 14089, A
	29	156	18.0	648	12	US-10-282-122A-13139	Sequence 13139, A
	30	155	17.9	465	12	US-10-282-122A-20692	Sequence 20692, A
	31	155	17.9	528	12	US-10-282-122A-38474	Sequence 38474, A
	32	152	17.6	436	12	US-10-282-122A-10758	Sequence 10758, A
	33	151	17.5	471	9	US-09-815-242-7717	Sequence 7717, Ap
	34	151	17.5	471	12	US-10-282-122A-30051	Sequence 30051, A
	35	150	17.3	465	12	US-10-282-122A-20841	Sequence 20841, A
	36	148	17.1	537	9	US-09-815-242-9396	Sequence 9396, Ap
	37	148	17.1	537	12	US-10-282-122A-37912	Sequence 37912, A
	38	146	16.9	439	9	US-09-974-300-6060	Sequence 6060, Ap
c	39	142.5	16.5	21040	12	US-10-158-844-55	Sequence 55, Appl
	40	138	16.0	438	9	US-09-974-300-1602	Sequence 1602, Ap

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:21:01 ; Search time 2365 Seconds
                                          (without alignments)
                                          2083.408 Million cell updates/sec

Title: US-09-955-315-2
Perfect score: 865
Sequence: 1 MANYTVPGINENDAKQLIDG..........EKFQWFIRAHIVDVDGNIQE 165

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext   0.5
                 Ygapop 10.0 , Ygapext   0.5
                 Fgapop 6.0 , Fgapext   7.0
                 Delop   6.0 , Delext   7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09955315/runat_19022004_145902_28339/app_query.fasta_1.3
27
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09955315_@CGN_1_1_1906_@runat_19022004_145902_28339 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*

```
12:   gb_est3:*
13:   gb_est4:*
14:   gb_est5:*
15:   em_estfun:*
16:   em_estom:*
17:   em_gss_hum:*
18:   em_gss_inv:*
19:   em_gss_pln:*
20:   em_gss_vrt:*
21:   em_gss_fun:*
22:   em_gss_mam:*
23:   em_gss_mus:*
24:   em_gss_pro:*
25:   em_gss_rod:*
26:   em_gss_phg:*
27:   em_gss_vrl:*
28:   gb_gss1:*
29:   gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	246	28.4	636	14	CF841965	CF841965 psHB017xA
c	2	246	28.4	679	14	CF851308	CF851308 psMA019xF
c	3	246	28.4	693	14	CF841926	CF841926 psHB016xM
c	4	246	28.4	694	14	CF851254	CF851254 psMA019xB
c	5	246	28.4	705	14	CF851365	CF851365 psMA019xH
c	6	221	25.5	742	12	BJ619993	BJ619993 BJ619993
c	7	189	21.8	607	12	BM415829	BM415829 OP20911 M
c	8	186	21.5	350	9	AU251612	AU251612 AU251612
	9	174	20.1	597	12	BM415925	BM415925 OP21007 M
	10	168.5	19.5	669	13	CA092935	CA092935 SCCCCL100
c	11	166	19.2	589	12	BM415853	BM415853 OP20935 M
	12	148	17.1	3137	11	BC009370	BC009370 Homo sapi
	13	144	16.6	736	9	AU168008	AU168008 AU168008
c	14	131	15.1	464	14	CF851326	CF851326 psMA019xF
	15	121	14.0	743	28	BZ562850	BZ562850 pacs2-164
	16	118	13.6	897	28	BH770759	BH770759 LLMGtag50
	17	102.5	11.8	1116	12	BM415949	BM415949 OP21031 M
c	18	96	11.1	676	14	CB854133	CB854133 UI-CF-DU1
c	19	96	11.1	688	14	CF891147	CF891147 UI-CF-DU1
	20	95.5	11.0	842	28	BZ571864	BZ571864 msh2_2090
c	21	92	10.6	369	14	W66612	W66612 me23b10.r1
	22	91.5	10.6	844	28	BZ571748	BZ571748 msh2_2038
	23	90.5	10.5	3526	11	AK054172	AK054172 Mus muscu
	24	90.5	10.5	4982	11	AK046971	AK046971 Mus muscu
	25	90	10.4	310	10	BE711894	BE711894 QV2-HT069
	26	87.5	10.1	675	12	BI109593	BI109593 602897552
c	27	87.5	10.1	1019	9	AL530716	AL530716 AL530716
	28	87	10.1	599	28	BZ304474	BZ304474 KD2968.p1
	29	87	10.1	2529	29	AY421056	AY421056 Homo sapi